

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 17:37:38 ; Search time 305.46 Seconds
(without alignments)
286.922 Million cell updates/sec

Title: US-09-502-984B-37
Perfect score: 1284
Sequence: 1 KRESKALLANGPELLECF.....RKNERLEEVERLKLQVGER 249

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep:*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep:*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep:*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep:*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep:*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	91.2	676	18	US-09-452-565-1
2	1098	85.5	211	19	US-09-502-984-6
3	1080	84.1	211	19	US-09-502-984-5
4	1078	84.0	211	19	US-09-502-984-4
5	1075	83.7	211	19	US-09-502-984-9
6	1073	83.6	211	19	US-09-502-984-13
7	1073	83.6	211	19	US-09-502-984-14

8	1073	83.6	211	19	US-09-502-984-15	Sequence 15, Appl
9	1070	83.3	211	19	US-09-502-984-7	Sequence 7, Appl
10	1070	83.3	211	19	US-09-502-984-17	Sequence 17, Appl
11	1066	83.0	211	19	US-09-502-984-16	Sequence 16, Appl
12	1064	82.9	211	19	US-09-502-984-11	Sequence 11, Appl
13	1061	82.6	211	19	US-09-502-984-12	Sequence 12, Appl
14	1060	82.6	211	19	US-09-502-984-2	Sequence 2, Appl
15	1060	82.6	211	19	US-09-502-984-10	Sequence 10, Appl
16	1060	82.6	225	17	US-09-502-984-1	Sequence 1, Appl
17	1060	82.6	438	17	US-09-339-888-5	Sequence 5, Appl
18	1060	82.6	488	8	US-08-474-673-2	Sequence 2, Appl
19	1060	82.6	488	13	US-08-960-733-2	Sequence 2, Appl
20	1059.5	82.5	212	19	US-09-502-984-3	Sequence 3, Appl
21	1057	82.3	220	18	US-09-452-565-6	Sequence 6, Appl
22	1057	82.3	268	18	US-09-452-565-3	Sequence 3, Appl
23	1053	82.0	211	19	US-09-502-984-8	Sequence 8, Appl
24	1053	82.0	508	14	US-09-016-159-5	Sequence 5, Appl
25	1053	82.0	508	14	US-09-058-429-5	Sequence 5, Appl
26	1052	81.9	438	17	US-09-339-838-7	Sequence 7, Appl
27	1048	81.6	211	19	US-09-502-984-18	Sequence 18, Appl
28	1039	80.9	211	19	US-09-502-984-19	Sequence 19, Appl
29	1034	80.5	211	19	US-09-502-984-20	Sequence 20, Appl
30	1025	79.8	211	19	US-09-502-984-21	Sequence 21, Appl
31	1025	79.8	211	19	US-09-502-984-24	Sequence 24, Appl
32	1024	79.8	211	19	US-09-502-984-25	Sequence 25, Appl
33	1022	79.6	211	19	US-09-502-984-23	Sequence 23, Appl
34	1020	79.4	211	19	US-09-502-984-22	Sequence 22, Appl
35	1020	79.4	211	19	US-09-502-984-26	Sequence 26, Appl
36	1019	79.4	211	19	US-09-502-984-28	Sequence 28, Appl
37	1009	78.6	211	19	US-09-502-984-27	Sequence 27, Appl
38	997	77.6	211	19	US-09-502-984-29	Sequence 29, Appl
39	973	36.8	165	1	PCT-US01-14827-13860	Sequence 13860, A
40	394	30.7	80	26	US-60-160-202-3517	Sequence 3517, Ap
41	260	20.2	53	26	US-60-160-202-4200	Sequence 4200, Ap
42	244	19.0	54	26	US-60-160-202-2419	Sequence 2419, Ap
43	173	13.5	50	26	US-60-182-094-1197	Sequence 1197, Ap
44	168	13.1	56	21	US-09-757-027-710	Sequence 710, App
45	167.5	13.0	117	16	US-09-206-647-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-452-565-1

Sequence 1, Application US/09452565

GENERAL INFORMATION:

APPLICANT: Anderson, Stephen F.

APPLICANT: Nash, Huw M.

APPLICANT: Pelsch, Jason S.

TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR CHIMERA

FILE REFERENCE: 10845/011001

CURRENT APPLICATION NUMBER: US/09/452,565

CURRENT FILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 676

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: -

OTHER INFORMATION: fusion protein including erythropoietin receptor extracellular domain, maltose binding proteins, linker, and GCMA leucine

OTHER INFORMATION: zipper domain

US-09-452-565-1

Query Match 91.2%; Score 1171; DB 18; Length 676;
Best Local Similarity 89.2%; Pred. No. 4.5e-109;
Matches 222; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 1 KRESKALLANGPELLECFERLEDLVCFEEAASAGVGNFSPFQLEDEPMKICRL 60

```
Db 428 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 487
QY 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
Db 488 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 547
QY 121 RLADSGHVIVIRMLPPETPMTHIRELDISAGNGAGSVQVRELLGRTCYLSNLGR 180
Db 548 RLADSGHVIVIRMLPPETPMTHIREVDVSNAGSVQVRELLGRTCYLSNLGR 607
QY 181 TRITIAVRAMAPRSGFGFWSAMSEPVSLTGGGSMELKQVLEKKNRLEEVE 240
Db 608 TRITIAVRAMAPRSGFGFWSAMSEPVSLTGGGSMELKQVLEKKNRLEEVE 667
QY 241 RLKOLVGR 249
Db 668 RLKOLVGR 676
```

```
RESULT 2
US-09-502-984-6
; Sequence 6, Application US/09502984
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120,009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131,674
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-6
```

```
Query Match 85.5%; Score 1098; DB 19; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.1e-102;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
Db 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
QY 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
Db 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
QY 121 RLADSGHVIVIRMLPPETPMTHIRELDISAGNGAGSVQVRELLGRTCYLSNLGR 180
Db 121 RLADSGHVIVIRMLPPETPMTHIRELDISAGNGAGSVQVRELLGRTCYLSNLGR 180
QY 181 TRITIAVRAMAPRSGFGFWSAMSEPVSLT 211
Db 181 TRITIAVRAMAPRSGFGFWSAMSEPVSLT 211
```

```
RESULT 3
US-09-502-984-5
; Sequence 5, Application US/09502984
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984
```

```
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120,009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131,674
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-5
```

```
Query Match 84.1%; Score 1080; DB 19; Length 211;
Best Local Similarity 97.2%; Pred. No. 1.4e-100;
Matches 205; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
Db 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
QY 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
Db 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
QY 121 RLADSGHVIVIRMLPPETPMTHIRELDISAGNGAGSVQVRELLGRTCYLSNLGR 180
Db 121 RLADSGHVIVIRMLPPETPMTHIRELDISAGNGAGSVQVRELLGRTCYLSNLGR 180
QY 181 TRITIAVRAMAPRSGFGFWSAMSEPVSLT 211
Db 181 TRITIAVRAMAPRSGFGFWSAMSEPVSLT 211
```

```
RESULT 4
US-09-502-984-4
; Sequence 4, Application US/09502984
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120,009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131,674
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-4
```

```
Query Match 84.0%; Score 1078; DB 19; Length 211;
Best Local Similarity 96.7%; Pred. No. 2.2e-100;
Matches 204; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
Db 1 KFEKSAALLAARGPEELCTERLEEDLYCFEEAASAGVPGNFSFQLEDEPMKLCRL 60
QY 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
Db 61 HQAPTARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRHRVYIHINEVLLDAPVGLVA 120
```

QY 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
DB 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
QY 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211
DB 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211

RESULT 5

US-09-502-984-9
Sequence 9, Application US/09502984
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RET/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,984
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-9

Query Match 83.7%; Score 1075; DB 19; Length 211;
Best Local Similarity 96.2%; Pred. No. 4, 5e-100;
Matches 203; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
DB 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
QY 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
DB 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
QY 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
DB 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
QY 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211
DB 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211

RESULT 6

US-09-502-984-13
Sequence 13, Application US/09502984
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RET/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,984
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-13

Query Match 83.6%; Score 1073; DB 19; Length 211;
Best Local Similarity 96.2%; Pred. No. 7, 2e-100;
Matches 203; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
DB 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
QY 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
DB 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
QY 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
DB 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
QY 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211
DB 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211

RESULT 7

US-09-502-984-14
Sequence 14, Application US/09502984
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RET/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,984
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 211
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-14

Query Match 83.6%; Score 1073; DB 19; Length 211;
Best Local Similarity 96.2%; Pred. No. 7, 2e-100;
Matches 203; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
DB 1 KESKAAALLAARGPEELLCTFERLEDVCFEEBAASAGVPGNFSFQLEDEPMKICRL 60
QY 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
DB 61 HOAPFARGAIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRYIHINEVLLDAPVGLVA 120
QY 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
DB 121 RLADSGHVIRMLPPETPMTSHIRFELDLSGNGAGSVQVRELLEGRTCVLSMLRGR 180
QY 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211
DB 181 TRTTFVARRAMAEPSFGFWSAMSEPVSLT 211

RESULT 8

US-09-502-984-15

```

: Sequence 15 Application US/09502984
: GENERAL INFORMATION:
: APPLICANT: Luo, Peizhi
: TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
: FILE REFERENCE: A-68126-1/RPT/RMS/RMK
: CURRENT APPLICATION NUMBER: US/09/502,984
: CURRENT FILING DATE: 2000-02-11
: PRIOR APPLICATION NUMBER: 60/120,009
: PRIOR FILING DATE: 1999-02-11
: PRIOR APPLICATION NUMBER: 60/131,674
: PRIOR FILING DATE: 1999-04-29
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 15
: LENGTH: 211
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-15

```

	Query Match	83.6%	Score 1073;	DB 19;	Length 211;
	Best Local Similarity	96.2%	Pred. No. 7.2e-100;		
	Matches 203;	Conservative 6;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	KEESKALLAARGPPELLCTFTRLEDVLCFEEAASAGVPGPNSFSFQLEDEPMKRLCT	60		
Db	1	KFESKALLAARGPELLCTFTRLEDVLCFEEAASAGVPGPNSFSFQLEDEPMKRLCT	60		
QY	61	HOAPARAIRFWCSLPADTSSFVPLRLRTAASGAPRHRVTHINEVYLLDAPGLVA	120		
Db	61	HOAPARAIRFWCSLPADTSSFVPLRLRTAASGAPRHRVTHINEVYLLDAPGLVA	120		
QY	121	RLADSGHVIVRWLPPEPMPMTHIRFELDVSAGAGASGVQVLEEGTECVLSNLRGR	180		
Db	121	RLADSGHVIVRWLPPEPMPMTHIRFELDVSAGAGASGVQVLEEGTECVLSNLRGR	180		

```

Qy      181 TRITIAVRARMAEPSEFGGFWASWASEPVSLLT 2111
          || | | | | | | | | | | | | | | | | | |
Db      181 TRYTFAVRARMAEPSEFGGFWASWASEPVSLLT 2111

```

```

RESULT          9
US-09-502-984-7
; Sequence 7, Application US/09502984
; GENERAL INFORMATION:
;   APPLICANT: Luo, Peizhi
;   TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
;   FILE REFERENCE: A-68126-1/RTT/BMS/RMK
;   CURRENT APPLICATION NUMBER: US/09/502,984
;   CURRENT FILING DATE: 2000-02-11
;   PRIOR APPLICATION NUMBER: 60/120,009
;   PRIOR FILING DATE: 1999-02-11
;   PRIOR APPLICATION NUMBER: 60/131,674
;   PRIOR FILING DATE: 1999-04-29
;   NUMBER OF SEQ. ID NOS: 36
;   SOFTWARE: Patent In Ver. 2.1
;   SEQ ID NO 7
;     LENGTH: 211
;     TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
;   US-09-502-984-7

```

Query Match	83.3%	Score 1070;	DB 19;	Length 211;
Best Local Similarity	95.7%	Pred. No. 1.5e-99;		
Matches 202; Conservative	7;	Mismatches	2;	Indels 0;
				Gaps 0;
QY	1	KFESEAALLARGPPELLCTFRLEDVYCFPEASAGVGNESFSFÖLEDEPKKCL	60	

```

Db      1  KFSKKAALLAARGPEELICFTEERLEEDLVCEWEENASAGVPGNFSFQIODEDEPMKICRL 60
Qy      61  HQAFTARGAIFKWSLTPTDISSFPVPLELRITAAAGAPRRHRYIHINEVLLDAPGCLA 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  HQAFTARGAIFKWSLTPTDISSFPVPLELRITAAAGAPRRHRYIHINEVLLDAPGCLA 120
Qy      121  RLADSGGVIVRWLPPEPTPTMTHIRPELDISAGNGASQVORELLGRTCVLSNLGR 180
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      121  RLADSGGVIVRWLPPEPTPTMTHIRPELDISAGNGASQVORELLGRTCVLSNLGR 180
Qy      181  TRITIAVARMAEBSFGGFMASMEPVSLLT 211
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      181  TRITIAVARMAEBSFGGFMASMEPVSLLT 211

```

```

: RESULT 10
: US-09-502-984-17
: Sequence 17, Application US/09502984
: GENERAL INFORMATION:
: APPLICANT: Luo, Peizhi
: TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
: FILE REFERENCE: A-68126-1/RPT/RMS/RMK
: CURRENT APPLICATION NUMBER: US/09/502,984
: CURRENT FILING DATE: 2000-02-11
: PRIOR APPLICATION NUMBER: 60/120,009
: PRIOR FILING DATE: 1999-02-11
: PRIOR APPLICATION NUMBER: 60/131,674
: PRIOR FILING DATE: 1999-04-29
: NUMBER OF SEQ. ID NOS: 36
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 17
: LENGTH: 211
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
: US-09-502-984-17

```

Query Match	83.3%	Score 1070;	DB 19;	Length 211;
Best Local Similarity	94.3%	Pred. No. 1.5e-99;		
Matches 199;	Conservative 12;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	KFEKSAALLARGBELLICFERJEDJYCPEEKAASAGVGNGNSFFOFJEDDEPMKICRL	60
Db	1	KFEKSAALLARGBELLICFTERJEDJYCPEEKAASAGVGNGNSFFOFJEDDEPMKICRL	60
Qy	61	HOAPFARGAIFRWCISLPTADJSSFVPLELRJLTAASGAPRFRVHIHNEVLLDAPGVLA	120
Db	61	HOAPFARGAIFRWCISLPTADJSSFVPLELRJLTAASGAPRFRVHIHNEVLLDAPGVLA	120
Qy	121	RLADESGHVIVIRKMLPPETPMTSHIRRELDISAGNGAGSVQRYVELLEGRTCYLSNLGR	180
Db	121	RLADESGHVIVIRKMLPPETPMTSHIRRELDISAGNGAGSVQRYVELLEGRTCYLSNLGR	180
Qy	181	TRITLAIARARMAEBSFGGFWAMSEVPSSLT	211
Db	181	TRITLAIARARMAEBSFGGFWAMSEVPSSLT	211

```

RESULT 11
US-09-502-984-16
; Sequence 16, Application US/09502984
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120,009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131,674
; PRIOR FILING DATE: 1999-04-29

```

Query Match	82.6%;	Score 1060;	DB 19;	Length 211;
Best Local Similarity	93.8%;	Pred. No. 1.5e-98;		

Matches 198; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 KFSKKAALLAARGPEELICTERLEDLYCFEEBAASAGVGNFSFQLEDEPMKLCRL 60
    |||||
Db 1 KFSKKAALLAARGPEELICTERLEDLYCFEEBAASAGVGNFSFQLEDEPMKLCRL 60
    |||||
QY 61 HQAPTARGAIRFCSLPTADTSSFVPLELRITAAAGAPRHRVYIHINEVYLLDAPVGLVA 120
    |||||
Db 61 HQAPTARGAIRFCSLPTADTSSFVPLELRITAAAGAPRHRVYIHINEVYLLDAPVGLVA 120
    |||||
QY 121 RLADSGHVYIRLPPPEPMTSHIRPELDISAGNGAGSVQRYELLEGRTECVLSNLRGR 180
    |||||
Db 121 RLADSGHVYIRLPPPEPMTSHIRPELDISAGNGAGSVQRYELLEGRTECVLSNLRGR 180
    |||||
QY 181 TRITIAVRAMAEPSFGFWSANSEPVSLT 211
    |||
Db 181 TRITIAVRAMAEPSFGFWSANSEPVSLT 211
    |||
```

RESULT 15

```
US-09-502-984-10
; Sequence 10, Application US/09502984
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120,009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131,674
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984-10
```

Query Match 82.6%; Score 1060; DB 19; Length 211;
Best Local Similarity 93.8%; Pred. No. 1.5e-98;

Matches 198; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 KFSKKAALLAARGPEELICTERLEDLYCFEEBAASAGVGNFSFQLEDEPMKLCRL 60
    |||||
Db 1 KFSKKAALLAARGPEELICTERLEDLYCFEEBAASAGVGNFSFQLEDEPMKLCRL 60
    |||||
QY 61 HQAPTARGAIRFCSLPTADTSSFVPLELRITAAAGAPRHRVYIHINEVYLLDAPVGLVA 120
    |||||
Db 61 HQAPTARGAIRFCSLPTADTSSFVPLELRITAAAGAPRHRVYIHINEVYLLDAPVGLVA 120
    |||||
QY 121 RLADSGHVYIRLPPPEPMTSHIRPELDISAGNGAGSVQRYELLEGRTECVLSNLRGR 180
    |||||
Db 121 RLADSGHVYIRLPPPEPMTSHIRPELDISAGNGAGSVQRYELLEGRTECVLSNLRGR 180
    |||||
QY 181 TRITIAVRAMAEPSFGFWSANSEPVSLT 211
    |||
Db 181 TRITIAVRAMAEPSFGFWSANSEPVSLT 211
    |||
```

Search completed: August 28, 2002, 17:37:39
Job time: 515 sec